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uauuuauuua uuuauuuauu 20

1. A method of identifying a protein kinase inhibitor for normalizing post-transcriptional regulation as precision cancer therapy comprising the following steps:

a) transfecting cancer cells or a tissue of a cancer patient with at least one expression vector comprising:

i) a promoter region comprising a non-inducible constitutively active ribosomal protein gene promoter;

ii) a reporter gene; and

iii) a 3' untranslated region (3' UTR) containing an AU-rich element, wherein said reporter gene is operably linked to said promoter region and said 3' UTR;

b) providing one or more protein kinase inhibitor(s) to be tested;

c), incubating the cells or a tissue created in step a) with said one or more protein kinase inhibitor(s) to be tested;

d) determining a normalizing effect of said one or more protein kinase inhibitor(s) on post-transcriptional regulation by determining a reporter activity, wherein a reduction in reporter activity indicates that said one or more protein kinase inhibitor(s) is/are suitable for targeted cancer therapy.

2. The method according to claim **1**, wherein the precision cancer therapy is a pan-cancer precision oncology therapy capable of treating a cancer regardless of the tissue type or subtype or molecular sub-type of the cancer.

3. The method according to claim **1**, where the precision cancer therapy is a universal single assay.

4. The method according to claim **1**, wherein said protein kinase inhibitor is co-administered with a chemotherapeutic agent, checkpoint inhibitor, therapeutic monoclonal antibody, interferon, cytokine inhibitor, and/or a small molecule drug.

5. The method according to claim **4**, wherein said checkpoint inhibitor is selected from CTLA-4, PD-1, and PD-L1 targeting agents.

6. The method according to claim **4**, wherein said checkpoint inhibitor is selected from the group consisting of ipilimumab, tremelimumab, nivolumab, MK-3475, MPDL-3280A, MEDI-4736, and BMS-936559.

7. The method according claim **1**, wherein, in said precision cancer therapy, a cancer-related gene is post-transcriptionally normalized by administering said protein kinase inhibitor.

8. The method according claim **1**, wherein, in said precision cancer therapy, a gene encoding a proinflammatory cytokine is post-transcriptionally normalized by administering said protein kinase inhibitor.

9. The method according to claim **7**, wherein said administering of said protein kinase inhibitor results in a reduction of expression of a mRNA comprising an AU-rich element.

10. The method according to claim **1**, wherein said protein kinase inhibitor is selected from inhibitors of kinases of which a kinase activity is aberrant in cancer.

11. The method according to claim **1**, wherein the promoter comprises a modified promoter of the human RPS30 gene that has the nucleic acid sequence of SEQ ID NO:3 (RPS30M1) or SEQ ID NO:4 (RPS30M-truncated).

12. The method according to claim **1**, wherein the reduction is a reduction by at least 20%.

13. The method, according to claim **2**, wherein the cancer is selected from solid tumors, hematological tumors, leukemias, lymphomas, and organic-specific tumors.

14. The method according to claim **13**, wherein the organic-specific tumor is a breast, colon, prostate or liver tumor.

15. The method according to claim **2**, wherein the cancer is a metastatic tumor.

16. The method according to claim **15**, wherein the metastatic cancer is hormone negative, Microsatellite Instability high or low, or p53 mutant cancer.

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